



SEQUENCE LISTING

<110> Ress-Loeschke, Marion
Friedrich, Thomas
Hauer, Bernhard

<120> A process for preparing chiral carboxylic acids
from nitriles using a nitrilase or microorganisms
which comprise a gene for the nitrilase

<130> 49462

<140> US 09/806,876

<141> 2001-05-21

<150> Germany/19848129.2

<151> 1998-10-19

<160> 9

<170> WordPerfect version 6.1

<210> 1

<211> 1071

<212> DNA

<213> *Alcaligenes faecalis*

<220>

<221> CDS

<222> 1 ... 1071

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Met Gln Thr Arg Lys Ile Val Arg Ala Ala Val Gln Ala Ala Ser
1 5 10 15

ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct 96
Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
20 25 30

cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc 144
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
35 40 45

tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg 192
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
50 55 60

tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac 240
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
65 70 75 80

105040-92890860

agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att 288
 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
 85 90 95

ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg 336
 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
 100 105 110

ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc 384
 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
 115 120 125

aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat 432
 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
 130 135 140

gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct 480
 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
 145 150 155 160

cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac 528
 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
 165 170 175

tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta 576
 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
 180 185 190

tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc 624
 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
 195 200 205

tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc 672
 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
 210 215 220

agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac 720
 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
 225 230 235 240

aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg 768
 Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
 245 250 255

ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc 816
 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
 260 265 270

ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg 864
 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
 275 280 285

09806876-040504
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atc aat gac ccc gta ggc cac tat tcc aaa ccc gag gcc acc cgt ctg 912
 ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
 290 295 300

gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa 960
 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
 305 310 315 320

agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att 1008
 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
 325 330 335

gcc tca gtc gct atc agc cat cca cag gac tgc gac aca ctg cta gtg 1056
 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
 340 345 350

caa gag ccg tct tga 1071
 Gln Glu Pro Ser
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<213> *Alcaligenes faecalis*

<400> 2

Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
 1 5 10 15

Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
 20 25 30

Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
 35 40 45

Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
 50 55 60

Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
 65 70 75 80

Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
 85 90 95

Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
 100 105 110

Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
 115 120 125

105040-94390860

Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
130 135 140

Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
145 150 155 160

Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
165 170 175

Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
180 185 190

Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
195 200 205

Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
210 215 220

Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
225 230 235 240

Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
245 250 255

Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
260 265 270

Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
275 280 285

Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
290 295 300

Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
305 310 315 320

Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
325 330 335

Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
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Gln Glu Pro Ser
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<211> 39

<212> PRT

<213> *Alcaligenes faecalis*

<400> 3

09806876-040501

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Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
 20 25 30

Arg Gln Ala Arg Asp Glu Gly
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<210> 4
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 <212> PRT
 <213> *Alcaligenes faecalis*

<400> 4

Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile Ala Ser Val Ala
 1 5 10 15

Ile Ser His Pro Gln
 20

<210> 5
 <211> 11
 <212> PRT
 <213> *Alcaligenes faecalis*

<400> 5

Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys
 1 5 10

<210> 6
 <211> 23
 <212> DNA
 <213> *Alcaligenes faecalis*

<220>
 <221> Unsure
 <222> 1 ... 23
 <223> n represents g, a, t or c

<400> 6

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23

<210> 7

0030336 040501
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<211> 20
 <212> DNA
 <213> *Alcaligenes faecalis*

 <220>
 <221> Unsure
 <222> 1 ... 20
 <223> n represents g, a, t or c

<400> 7

tngcsacnga ngcratcttg

20

<210> 8
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 <212> DNA
 <213> *Alcaligenes faecalis*

<400> 8

ttaatcatat gcagacaaga aaaatcgtcc g

31

<210> 9
 <211> 32
 <212> DNA
 <213> *Alcaligenes faecalis*

<400> 9

aaggatcctc aagacggctc ttgcactagc ag

32--

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